

ALIGNMENTS

ALIGNMENTS					
RESULT 1					
CLC3_CAVPO		STANDARD:		PRT: 760 AA.	
ID	CLC3_CAVPO				
AC	091279;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Chloride channel protein 3 (CLC-3).				
GN	CLCN3.				
OS	Cavia porcellus (Guinea pig)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.				
OX	NCBL-TaxID=10141;				
RN	11]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Small intestine;				
RA	Varela D., Cid L.P., Sepulveda F.V.;				
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.				
CC	-!- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME; MEMBRANE STABILIZATION, SIGNAL TRANSDUCTION AND TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-TERM MEMORY (BY SIMILARITY).				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-!- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.				
CC	-!- SIMILARITY: CONTAINS 2 CBS DOMAINS.				
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CC	-----				
DR	EMBL: AF133214; RADD3699; 1. -				
DR	InterPro: IPR000644; CBS_domain.				
DR	InterPro: IPR001807; CL-channel_volt.				
DR	Pfam: PF00571; CBS; 2.				
DR	Pfam: PF00654; voltage_CLC; 1.				
DR	PRINTS: PR00762; CLCHANNEL.				
DR	SMART: SM00116; CBS; 2.				
KW	Ionic channel; Ion transport; Voltage-gated channel; Transmembrane; CBS domain; Repeat.				
FT	TRANSMEM 68	POTENTIAL.			
FT	TRANSMEM 154	POTENTIAL.			
FT	TRANSMEM 175	POTENTIAL.			
FT	TRANSMEM 202	POTENTIAL.			
FT	TRANSMEM 259	POTENTIAL.			
FT	TRANSMEM 285	POTENTIAL.			
FT	TRANSMEM 330	POTENTIAL.			
FT	TRANSMEM 365	POTENTIAL.			
FT	TRANSMEM 442	POTENTIAL.			
FT	TRANSMEM 467	POTENTIAL.			

FT	TRANSMEM	508	528	POTENTIAL.
FT	TRANSMEM	536	556	POTENTIAL.
FT	DOMAIN	593	659	CBS 1.
FT	DOMAIN	696	747	CBS 2.
SQ	SEQUENCE	760 AA;	84485 MN;	BC2E2A5EBE60B3D CRC64;
Query Match		95.7%	Score 3997; DB 1; Length 760;	
Best local Similarity	99.7%	Pred. No. 2.5e-278;		
Matches	758;	Conservative 2;	Mismatches 0;	
		Indels 0;	Gaps 0;	
QY	32	MTNGGSTNSTHLDLDEPIPGVGTDFHTDWRECKDRERHRINSKKEWEM 91		
QY	1	MTNGGSTNSTHLDLDEPIPGVGTDFHTDWRECKDRERHRINSKKEWEM 60		
Db	152	TTEERDKCPQWTWAEELIGQAEPSIYIMNYIMYFWALSAFLAVSLVKVFAPYAG 211		
Db	121	TTEERDKCPQWTWAEELIGQAEPSIYIMNYIMYFWALSAFLAVSLVKVFAPYAG 180		
Db	241	SGPEIPEKILSGLFGTIRGYLGKWLMIKRTLVAVASGLSLGKREGPLVHVACCGNIFSY 271		
Db	181	SGPEIPEKILSGLFGTIRGYLGKWLMIKRTLVAVASGLSLGKREGPLVHVACCGNIFSY 240		
QY	272	LFPKYSTNEAKREVLASAAGVSVAFGAPIGGVLSLEEVYYFPLKTWRSSFAALL 331		
Db	301	AAFLRSNPFGNSRLVLFYVEYHTPWMLFELEPFLILGVFGGLWGAFFRANIAWRR 391		
QY	392	KSTPKFGKPVLEVITVAAATAVIAFPNPYTRLNTSELKEFLFDGPLESSLCDYNDM 451		
Db	361	KSTPKFGKPVLEVITVAAATAVIAFPNPYTRLNTSELKEFLTDGPLESSLCDYNDM 420		
QY	452	NASKIVDDIPDRAGIGVYSAIWQCLALIKIMTVFTFCIKVPSGLEIFPSMAIGAIG 511		
Db	421	NASKIVDDIPDRAGIGVYSAIWQCLALIKIMTVFTFCIKVPSGLEIFPSMAIGAIG 480		
QY	512	RIVGIAVEQLAYHHDWFITFKCENGADICTPGLYANVGAACLGGVTRMTSVLWIVF 571		
Db	481	RIVGIAVEQLAYHHDWFITFKCENGADICTPGLYANVGAACLGGVTRMTSVLWIVF 540		
QY	572	ELTGGLLEYIVPLMAVMWSKWQDAFGREGTYEAHTIRLYGFPLDAKEETHTLAADM 631		
Db	541	ELTGGLLEYIVPLMAVMWSKWQDAFGREGTYEAHTIRLYGFPLDAKEETHTLAADM 600		
QY	632	RPRRNDDPLPAVLTDQDNMVDIDENMINETSYNGFPVIMSKEOSRLVGFAERDLTAIES 691		
Db	601	RPRRNDDPLPAVLTDQDNMVDIDENMINETSYNGFPVIMSKEOSRLVGFAERDLTAIES 660		
QY	692	ARKKQEGIVGSSRVCFQAHPSIAPAESPRPLKRSILDMSPTVTDTTPMELVWDIFRKL 751		
Db	661	ARKKQEGIVGSSRVCFQAHPSIAPAESPRPLKRSILDMSPTVTDTTPMELVWDIFRKL 720		
QY	752	GLRQCLYTHNGRLGILTJKDILRHMAQTANQDPASIMFN 791		
Db	721	GLRQCLYTHNGRLGILTJKDILRHMAQTANQDPASIMFN 760		
RESULT 2				
CIC3_MOUSE	ID	CLC3_MOUSE	STANDARD;	PR1; 760 AA.
AC	P31791;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	chloride channel protein 3 (CLC-3);			
GN	CLCN3 OR CLC3 (Mouse).			
OS	MUS musculus (Mouse).			
Query Match		95.7%	Score 3996; DB 1; Length 760;	
Best local Similarity	99.7%	Pred. No. 3e-278;		
Matches	758;	Conservative 2;	Mismatches 0;	
		Indels 0;	Gaps 0;	
QY	32	MTNGGSTNSTHLDLDEPIPGVGTDFHTDWRECKDRERHRINSKKEWEM 91		
Db	1	MTNGGSTNSTHLDLDEPIPGVGTDFHTDWRECKDRERHRINSKKEWEM 60		

QY	92	TKSILYDANGWLVLTIGLASSALAGLAGLIDIAADMWTDLKEGICLSALWNHEOCWSNE	151	CC	SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
Db	61	TKSLYDANGWLVLTIGLASSALAGLAGLIDIAADMWTDLKEGICLSALWNHEOCWSNE	120	CC	MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
QY	152	TTFEERDKCPOWKWAELITIGQAEGPGSYIMNTIMYIWALSAFLAVSLVKVFPAYAG	211	CC	TRANSEPITHELIAL TRANSPORT, MAY PLAY AN IMPORTANT ROLE IN NEURONAL
Db	121	TTFEERDKCPOWKWAELITIGQAEGPGSYIMNTIMYIWALSAFLAVSLVKVFPAYAG	180	CC	CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
QY	212	SGIPEIKTLISGLFGIRGLKGKWLMIKTTILVLAVASGLSGLGEGPLVHVAACCGNFSY	271	CC	PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
Db	181	SGIPEIKTLISGLFGIRGLKGKWLMIKTTILVLAVASGLSGLGEGPLVHVAACCGNFSY	240	CC	TERM MEMORY.
QY	272	LFPKYSTNEAKKREVLSSASAAGSVARGAPGGVLFSEEVYYFPKLWRSFFAALV	331	CC	-!! SUBCELLULAR LOCATION: Integral membrane protein.
Db	241	LFPKYSTNEAKKREVLSSASAAGSVARGAPGGVLFSEEVYYFPKLWRSFFAALV	300	CC	-!! TISSUE SPECIFICITY: ABUNDANT IN BRAIN, ESPECIALLY IN THE OLFACTORY
QY	332	AAFVLRSLNPFGNSRLVLFYVEHTPWLFLFELPFILLGVFGGLWGAFFIRANIAWCRR	391	CC	BULB, HIPPOCAMPS, AND CEREBELLUM. A MODERATE EXPRESSION IS SEEN
Db	301	AAFVLRSLNPFGNSRLVLFYVEHTPWLFLFELPFILLGVFGGLWGAFFIRANIAWCRR	360	CC	IN THE LUNG, KIDNEY AND ADRENAL GLAND.
QY	392	KSTFRKGKIPVLEVITVIAITAVIAFPNPyTRMTSELKELFDGPLESSSCDYRND	451	CC	-!! SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
Db	361	KSTFRKGKIPVLEVITVIAITAVIAFPNPyTRMTSELKELFDGPLESSSCDYRND	420	CC	-!! SIMILARITY: CONTAINS 2 CBS DOMAINS.
QY	452	NASKVDIDPDRAGIGYSATWOLCLALIFKIMTPTFGIKVPSGLFIPSMAGTAG	511	CC	-----
Db	421	NASKVDIDPDRAGIGYSATWOLCLALIFKIMTPTFGIKVPSGLFIPSMAGTAG	480	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
QY	512	RIVGIAVQOLAYVHHDWLIFKENCEVGADCTPGLYANVGAACLGGVTRMTVSLVVIF	571	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
Db	481	RIVGIAVQOLAYVHHDWLIFKENCEVGADCTPGLYANVGAACLGGVTRMTVSLVVIF	540	CC	the European Bioinformatics Institute. There are no restrictions on its
QY	572	ELTGGLETYIVPLMAAMVTSKWKWGDAGFREGGIYAHIRLNGYPPFLDAKEEFTHTLAADM	631	CC	use by non-profit institutions as long as its content is in no way
Db	541	ELTGGLETYIVPLMAAMVTSKWKWGDAGFREGGIYAHIRLNGYPPFLDAKEEFTHTLAADM	600	CC	modified and this statement is not removed. Usage by and for commercial
QY	632	RPRRNDDPLAVLITQDMNTDLENMINITSYNGFPVIMSRESORLVGFLARDLTIAES	691	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)
Db	601	RPRRSDDPLAVLITQDMNTDLENMINITSYNGFPVIMSRESORLVGFLARDLTIAES	660	CC	or send an email to license@isb-sib.ch).
QY	692	ARKKQEGIYGSSRVCAFOHTPSLPAESPRPLKRSILDMSPFVTDTHPMEIVWDIRKL	751	CC	-----
Db	661	ARKKQEGIYGSSRVCAFOHTPSLPAESPRPLKRSILDMSPFVTDTHPMEIVWDIRKL	720	CC	EMBL; D17521; BAA0471; -----
QY	752	GLRQCLVTHNGLRGLGITKKDILRHMAOTANODPASMEN	791	CC	InterPro; IPR000644; CBS-domain.
Db	721	GLRQCLVTHNGLRGLGITKKDILRHMAOTANODPASMEN	760	CC	DR InterPro; IPR001807; CL-channel_volt.
RESULT 3					
CLC3_RAT	STANDARD;	PRT;	760 AA.	DR	Pfam; PF00571; CBS; 2.
AC	P51792;			DR	PF00656; voltage_CLC; 1.
DT	01-OCT-1996 (Rel. 34, Last sequence update)			DR	PRINTS; PR00762; CLCHANNEL.
DE	15-JUN-2002 (Rel. 41, Last annotation update)			SMART; SM00116; CBS; 2.	
GN	CLC3.			IONIC CHANNEL; Ion transport; Voltage-gated channel; Transmembrane; KW domain; Repeat.	
OS	Rattus norvegicus (Rat).			FT	TRANSMEM 68 88 POTENTIAL.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			FT	TRANSMEM 154 174 POTENTIAL.
OX	NCBI_TaxId=10116;			FT	TRANSMEM 195 195 POTENTIAL.
RN	[1]			FT	TRANSMEM 202 222 POTENTIAL.
RP	SEQUENCE FROM N.A.			FT	TRANSMEM 259 279 POTENTIAL.
RC	TISSUE=kidney;			FT	TRANSMEM 285 305 POTENTIAL.
RX	MEDLINE:94200538; PubMed=8155321;			FT	TRANSMEM 330 350 POTENTIAL.
RA	Kawasaki M., Uchida S., Monkawa T., Miyawaki A., Mikoshiba K., Marumo F., Sasaki S.,			FT	TRANSMEM 365 385 POTENTIAL.
RT	Cloning and expression of a protein kinase C-regulated chloride channel abundantly expressed in rat brain neuronal cells ";			FT	TRANSMEM 442 462 POTENTIAL.
RL	Neuron 12:597-604(1994);			FT	TRANSMEM 467 487 POTENTIAL.

QY	32	MNTGGSTNSTHLLDLDPEPGVGTYDDFHTIDWRECKKDRERRRRINKKESAWEM	91	CC	TRANSMEM 508 528 POTENTIAL.
Db	1	MNTGGSNSTHLLDLDPEPGVGTYDDFHTIDWRECKKDRERRRRINKKESAWEM	60	CC	TRANSMEM 536 556 POTENTIAL.
QY	92	TKSLYDANGWLVLTIGLASSALAGLAGLIDIAADMWTDLKEGICLSALWNHEOCWSNE	151	CC	TRANSMEM 599 659 CBS 1.
Db	61	TKSLYDANGWLVLTIGLASSALAGLAGLIDIAADMWTDLKEGICLSALWNHEOCWSNE	120	CC	TRANSMEM 696 747 CBS 2.
QY	152	TTFEERDKCPOWKWAELITIGQAEGPGSYIMNTIMYIWALSAFLAVSLVKVFPAYAG	211	CC	SEQUENCE 760 AA; 8A826FC2497269C CRC64:

QY	32	MNTGGSTNSTHLLDLDPEPGVGTYDDFHTIDWRECKKDRERRRRINKKESAWEM	91	CC	Query Match 95.6%; Score 3994; DB 1; Length 760;
Db	1	MNTGGSNSTHLLDLDPEPGVGTYDDFHTIDWRECKKDRERRRRINKKESAWEM	60	CC	Best Local Similarity 99.5%; Pred. No. 4; Length 760;
QY	92	TKSLYDANGWLVLTIGLASSALAGLAGLIDIAADMWTDLKEGICLSALWNHEOCWSNE	151	CC	Matches 756; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
Db	61	TKSLYDANGWLVLTIGLASSALAGLAGLIDIAADMWTDLKEGICLSALWNHEOCWSNE	120	CC	-----
QY	121	TTFEERDKCPOWKWAELITIGQAEGPGSYIMNTIMYIWALSAFLAVSLVKVFPAYAG	180	CC	-----
Db	212	SGIPEIKTLISGLFGIRGLKGKWLMIKTTILVLAVASGLSGLGEGPLVHVAACCGNFSY	271	CC	-----
Db	181	SGIPEIKTLISGLFGIRGLKGKWLMIKTTILVLAVASGLSGLGEGPLVHVAACCGNFSY	240	CC	-----
QY	272	LFPKYSTNEAKKREVLSSASAAGSVARGAPGGVLFSEEVYYFPKLWRSFFAALV	331	CC	-----
Db	241	LFPKYSTNEAKKREVLSSASAAGSVARGAPGGVLFSEEVYYFPKLWRSFFAALV	300	CC	-----
QY	332	AAFVLRSLNPFGNSRLVLFYVEHTPWLFLFELPFILLGVFGGLWGAFFIRANIAWCRR	391	CC	-----
Db	301	AAFVLRSLNPFGNSRLVLFYVEHTPWLFLFELPFILLGVFGGLWGAFFIRANIAWCRR	360	CC	-----

-!- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE

QY 392 KSTKKGKPYLEVITVAAITAVIAFPNPYTRLNTSLIKEFLTDGPLESSLCIQRNDM 451
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC CELLS, AND AORTIC ENDOTHELIAL CELLS, ALSO EXPRESSED IN TRACHEAL
 Db 361 KSTKKGKPYLEVITVAAITAVIAFPNPYTRLNTSLIKEFLTDGPLESSLCIQRNDM 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC AND ALVEOLAR EPITHELIAL CELLS, AND INTIMA AND MEDIA OF THE
 QY 452 NASKTVDDIPDRPAGIGVYSIWQLCLALIFKIMWVFTFGIKVSGLFIPSMAIGAAG 511
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC PULMONARY VESSELS.
 Db 421 NASKTVDDIPDRPAGIGVYSIWQLCLALIFKIMWVFTFGIKVSGLFIPSMAIGAAG 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC -!- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 QY 512 RIVGTAVEQLAYYHDFIFREWCEVGADCTPGYAMVGRACIGGVTMTVSIVVIF 571
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC !- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 Db 481 RIVGTAVEQLAYYHDFIFREWCEVGADCTPGYAMVGRACIGGVTMTVSIVVIF 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 QY 572 ELTGLEYIVPLMAVNTSKVGDGFREGIYEAHIRLNGPFDAKEEFTHTLAADM 631
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 Db 541 ELTGLEYIVPLMAVNTSKVGDGFREGIYEAHIRLNGPFDAKEEFTHTLAADM 600
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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 QY 632 RPRRNIDPPLAVLTQDMVDDIENNINETSYNGFPVMSKESQRVGFALKRDLTTAES 691
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC or send an email to licensee@ib-sib.ch).
 Db 601 RPRRNIDPPLAVLTQDMVDDIENNINETSYNGFPVMSKESQRVGFALKRDLTTAES 660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC CC CC DR EMBL; X78520; CA55280.1; ALT_INIT.
 DR EMBL; X78520; CA55280.1; ALT_INIT.
 DR Genew; HGNC; 2021; CLCN3.
 DR MIM; 600580; -.
 DR Interrpro; IPR000644; CBS domain.
 DR Interpro; IPR001807; Cl-channel_volt..
 DR Pfam; PF00571; CBS; 2.
 DR PRINTS; PRO767; CLCHANNEL.
 DR SMART; SM0016; CBS; 2.
 KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
 CLC3_HUMAN STANDARD; PRT; 762 AA.
 ID CLC3_HUMAN PRT; 762 AA.
 AC P51790;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1995 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chloride channel protein 3 (CLC-3).
 GN CLCN3.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N A.
 RC TISSUE_Retina;
 MEDLINE=93394419; PubMed=7665360;
 RA Borsig G., Rigarini E.I., Tagliafata M., Wong C., Ballabio A.;
 RT "Characterization of a human and murine gene (CLC3) sharing
 RT similarities to voltage-gated chloride channels and to a yeast
 RT integral membrane protein";
 RL Genomics 27:131-141(1995).
 RN [2]
 RP TISSUE_SPECIFICITY.
 RC TISSUE_Vascular_smooth_muscle; Aortic endothelium; and Fetal lung;
 MEDLINE=93222497; PubMed=1018915;
 RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,
 Schutte B.C.,
 RT "Expression of CLCN voltage-gated chloride channel genes in human
 RT blood vessels";
 RL Mol. Cell. Cardiol. 31:657-666(1999).
 CC FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 TRANSPETHALINE TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL
 CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY
 PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT-
 TERM MEMORY.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE_SPECIFICITY: EXPRESSED PRIMARILY IN TISSUES DERIVED FROM
 NEUROCTODERM. WITHIN THE BRAIN, ITS EXPRESSION IS PARTICULARLY
 EVIDENT IN THE HIPPOCAMPUS, OLFACTORY CORTEX, AND OLFACTORY BULB.
 CC HIGHLY EXPRESSED IN AORTIC AND CORONARY VASCULAR SMOOTH MUSCLE.

RESULT 4

CLC3_HUMAN	STANDARD;	PRT;	762 AA.
P51790;			
DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1995 (Rel. 34, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Chloride channel protein 3 (CLC-3).			
GN CLCN3.			
OS Homo sapiens (Human).			
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX NCBI_TAXID=9606;			
RN [1]			
RP SEQUENCE FROM N A.			
RC TISSUE_Retina;			
MEDLINE=93394419; PubMed=7665360;			
RA Borsig G., Rigarini E.I., Tagliafata M., Wong C., Ballabio A.;			
RT "Characterization of a human and murine gene (CLC3) sharing RT similarities to voltage-gated chloride channels and to a yeast RT integral membrane protein";			
RL Genomics 27:131-141(1995). <td></td> <td></td> <td></td>			
RN [2]			
RP TISSUE_SPECIFICITY.			
RC TISSUE_Vascular_smooth_muscle; Aortic endothelium; and Fetal lung;			
MEDLINE=93222497; PubMed=1018915;			
RA Lamb F.S., Clayton G.H., Liu B.-X., Smith R.L., Barna T.J.,			
Schutte B.C.,			
RT "Expression of CLCN voltage-gated chloride channel genes in human RT blood vessels";			
RL Mol. Cell. Cardiol. 31:657-666(1999). <td></td> <td></td> <td></td>			
CC FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME; MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSPETHALINE TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN NEURONAL CELL FUNCTION THROUGH REGULATION OF MEMBRANE EXCITABILITY BY PROTEIN KINASE C. IT COULD HELP NEURONAL CELLS TO ESTABLISH SHORT- TERM MEMORY.			
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.			
CC -!- TISSUE_SPECIFICITY: EXPRESSED PRIMARILY IN TISSUES DERIVED FROM NEUROCTODERM. WITHIN THE BRAIN, ITS EXPRESSION IS PARTICULARLY EVIDENT IN THE HIPPOCAMPUS, OLFACTORY CORTEX, AND OLFACTORY BULB.			
CC HIGHLY EXPRESSED IN AORTIC AND CORONARY VASCULAR SMOOTH MUSCLE.			

Query Match 95 %; Score 3991; DB 1; Length 762;
 Best Local Similarity 99.7%; Pred. No. 6. 8e-278; Indels 2; Gaps 1;
 Matches 760; Conservative 0; Mismatches 0; Indexes 2;

QY 32 MTNGGSINSSTHLUDLDEPTPGVYTYDHTIDMVREKCKDRERRRHRRNSKKESAWM 91
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MTNGGSINSSTHLUDLDEPTPGVYTYDHTIDMVREKCKDRERRRHRRNSKKESAWM 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 92 TKSLYDAWSGLWVWLTLGLASAGLAGLIDIAADWMTDLKEGICLUSALWNHEOCWGSE 151
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 TKSLYDAWSGLWVWLTLGLASAGLAGLIDIAADWMTDLKEGICLUSALWNHEOCWGSE 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 152 TPFEEKDCKQWKLWQELITLGQAEPSGYMMYIWFWALSFLAVSLVKAFCYAC 211
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 TFEERDKCQWKLWQELITLGQAEPSGYMMYIWFWALSFLAVSLVKAFCYAC 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 212 SGPEIETLISGFLIRGLYLGKWTLMKTTLVLAVASGLSGKGPLVIVACCGNFSY 271
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 SGPEIETLISGFLIRGLYLGKWTLMKTTLVLAVASGLSGKGPLVIVACCGNFSY 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 272 LFPKVSTNEAKKREVLSAASAAGSVAFGAPPIGGVLSLEEVSYFPLKTLWSFFAALV 331
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 LFPKVSTNEAKKREVLSAASAAGSVAFGAPPIGGVLSLEEVSYFPLKTLWSFFAALV 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 332 AAFVRSINFNGSLVLFVEYHFWLFLPFLGVGGWAFIRANIAWCRR 391
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 AAFVRSINFNGSLVLFVEYHFWLFLPFLGVGGWAFIRANIAWCRR 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 392 KSTKKGKPYLEVITVAAITAVIAFPNPYTRLNTSELKEFLTDGPLESSLCIQRNDM 451
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC 361 KSTKKGKPYLEVITVAAITAVIAFPNPYTRLNTSELKEFLTDGPLESSLCIQRNDM 420
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db	421	NMTRPVVDDIPDRAGVGYTAMQQLALIFKIVWTITFGMKIPSGLIFIPSMAVGAIG	480	FT	TRANSMEM	246	266	POTENTIAL.
Qy	512	RIVGIAVEOLAYVHHDWTFIKWCEVGADCTPGLYAMYGAACLGSGVTRMTVSLVIVE	571	FT	TRANSMEM	317	337	POTENTIAL.
Db	481	RMVGIGVQEOLAYHHDWIFRNWCRCGADCVPGLYAMVGAACLGSGVTRMTVSLVIMF	540	FT	TRANSMEM	352	372	POTENTIAL.
Qy	572	ELTGCGLEYIIPMAMVMSKKGDAFGREGTYEAHTRLNGYPPLDAEEFTHTLAADM	631	FT	TRANSMEM	429	449	POTENTIAL.
Db	541	ELTGCGLEYITPLMAAVTSKVWADGKEGTYEAHTHLNGYPFLDVKEFTHRTLATDM	600	FT	TRANSMEM	454	474	POTENTIAL.
Qy	632	RPRRNDPLAVLTQDNMVDIENMINETSYNPVIMSKEQRLLVAFRLDITAES	691	FT	TRANSMEM	495	515	POTENTIAL.
Db	601	RPRRGEPPPLSVLTDMSMTVEDVETLKDITYGFPVVWSRDSERLLGFAQRRELLA	660	FT	TRANSMEM	522	542	POTENTIAL.
Qy	692	ARKKQEGIVGSSRVCFQAOTPSLFAESPRPLKRSILDMSPTVTDHMPMEIWDIFRK	751	FT	DOMAIN	586	646	CBS 1.
Db	661	ARQEQEGIVNSIMVTFEPEPLPANSFPLKLRLILNLSPLFTVTDHMPETVVDIFRK	720	FT	DOMAIN	684	734	CBS 2.
Qy	752	GLRQCLVHNRGAGLITTKDILRHMATQANOPASIMEN	791	SEQUENCE	747 AA;	83701 MN;	E86B573224BBA0C3	CRC64;
Db	721	GLRQCLVHNRGAGLITTKDILRHMATQANOPASIMEN	760					
RESULT 6								
CIC4_RAT		STANDARD;	PRT;	747 AA.	Query Match	77.6%	Score 3240;	DB 1; Length 747;
ID					Best Local Similarity	78.4%	Pred. No. 3_5e-24;	Indels 0; Gaps 0;
AC		P51794;			Matches 586; Conservative 81; Mismatches 80;			
DT	01-OCT-1996	(Rel. 34, Created)						
DT	01-OCT-1995	(Rel. 34, last sequence update)						
DT	15-JUN-2002	(Rel. 41, last annotation update)						
DE		Chloride channel protein 4 (CIC-4).						
GN	CIC4N							
OS	Rattus norvegicus (Rat).	Craniata; Vertebrata; Euteleostomi;						
OC	Eukaryota; Metazoa; Chordata; Sciuromorpha; Muridae; Murinae; Rattus.							
OX	NCBI_TaxID=10116;							
RN	[1]	SEQUENCE FROM N.A.						
RP		MEDLINE-95248463; PubMed=7730971;						
RX		Jentsch T.J., Guenther W., Pusch M., Schwappach B.;						
RA		Genes of voltage-gated chloride channels of the ClC gene family.",						
RT		J. PHYSIOL. (Lond.) 482:19-25 (1995).						
RL		FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME; MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSPERITHELIAL TRANSPORT.						
CC		-1- SUBCELLULAR LOCATION: Integral membrane protein						
CC		-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LIVER AND BRAIN, BUT ALSO IN HEART, MUSCLE, KIDNEY AND SPLEEN.						
CC		-1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.						
CC		-1- SIMILARITY: CONTAINS 2 CBS DOMAINS.						
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).						
CC		PRINTS; PRO00162; CICCHANNEL.						
DR		EMBL; Z36944; CA885406; 1; -.						
DR		Inte-Pro; IPR00564; CBS_domain.						
DR		InterPro; IPR001807; Cl-channel_volt.						
DR		PFAM; PF00571; CBS; 2.						
DR		PFAM; PF00554; voltage_CIC; 1.						
DR		SMART; SM00116; CBS; 2.						
KW		Ionic channel; Ion transport; Voltage-gated channel; Transmembrane; CBS domain; Repeat.						
FT	55	POTENTIAL.						
TRANSMEM	135	155	POTENTIAL.					
TRANSMEM	189	209	POTENTIAL.					
RESULT 7								
CIC4_MOUSE		STANDARD;	PRT;	747 AA.	FT	TRANSMEM	246	POTENTIAL.
ID	CIC4_MOUSE				FT	TRANSMEM	317	POTENTIAL.
AC	Q61418;				FT	TRANSMEM	352	POTENTIAL.
FT	13-JUL-1998 (Rel. 36, Created)				FT	TRANSMEM	429	POTENTIAL.
					FT	TRANSMEM	454	POTENTIAL.
					FT	TRANSMEM	495	POTENTIAL.
					FT	TRANSMEM	522	POTENTIAL.
					FT	TRANSMEM	586	POTENTIAL.
					FT	TRANSMEM	646	POTENTIAL.
					FT	TRANSMEM	734	POTENTIAL.
					FT	TRANSMEM	864	POTENTIAL.
					FT	TRANSMEM	920	POTENTIAL.
					FT	TRANSMEM	976	POTENTIAL.
					FT	TRANSMEM	1024	POTENTIAL.
					FT	TRANSMEM	1072	POTENTIAL.
					FT	TRANSMEM	1120	POTENTIAL.
					FT	TRANSMEM	1168	POTENTIAL.
					FT	TRANSMEM	1206	POTENTIAL.
					FT	TRANSMEM	1244	POTENTIAL.
					FT	TRANSMEM	1282	POTENTIAL.
					FT	TRANSMEM	1320	POTENTIAL.
					FT	TRANSMEM	1358	POTENTIAL.
					FT	TRANSMEM	1396	POTENTIAL.
					FT	TRANSMEM	1434	POTENTIAL.
					FT	TRANSMEM	1472	POTENTIAL.
					FT	TRANSMEM	1510	POTENTIAL.
					FT	TRANSMEM	1548	POTENTIAL.
					FT	TRANSMEM	1586	POTENTIAL.
					FT	TRANSMEM	1624	POTENTIAL.
					FT	TRANSMEM	1662	POTENTIAL.
					FT	TRANSMEM	1700	POTENTIAL.
					FT	TRANSMEM	1738	POTENTIAL.
					FT	TRANSMEM	1776	POTENTIAL.
					FT	TRANSMEM	1814	POTENTIAL.
					FT	TRANSMEM	1852	POTENTIAL.
					FT	TRANSMEM	1890	POTENTIAL.
					FT	TRANSMEM	1928	POTENTIAL.
					FT	TRANSMEM	1966	POTENTIAL.
					FT	TRANSMEM	2004	POTENTIAL.
					FT	TRANSMEM	2042	POTENTIAL.
					FT	TRANSMEM	2080	POTENTIAL.
					FT	TRANSMEM	2118	POTENTIAL.
					FT	TRANSMEM	2156	POTENTIAL.
					FT	TRANSMEM	2194	POTENTIAL.
					FT	TRANSMEM	2232	POTENTIAL.
					FT	TRANSMEM	2270	POTENTIAL.
					FT	TRANSMEM	2308	POTENTIAL.
					FT	TRANSMEM	2346	POTENTIAL.
					FT	TRANSMEM	2384	POTENTIAL.
					FT	TRANSMEM	2422	POTENTIAL.
					FT	TRANSMEM	2460	POTENTIAL.
					FT	TRANSMEM	2498	POTENTIAL.
					FT	TRANSMEM	2536	POTENTIAL.
					FT	TRANSMEM	2574	POTENTIAL.
					FT	TRANSMEM	2612	POTENTIAL.
					FT	TRANSMEM	2650	POTENTIAL.
					FT	TRANSMEM	2688	POTENTIAL.
					FT	TRANSMEM	2726	POTENTIAL.
					FT	TRANSMEM	2764	POTENTIAL.
					FT	TRANSMEM	2802	POTENTIAL.
					FT	TRANSMEM	2840	POTENTIAL.
					FT	TRANSMEM	2878	POTENTIAL.
					FT	TRANSMEM	2916	POTENTIAL.
					FT	TRANSMEM	2954	POTENTIAL.
					FT	TRANSMEM	2992	POTENTIAL.
					FT	TRANSMEM	3030	POTENTIAL.
					FT	TRANSMEM	3068	POTENTIAL.
					FT	TRANSMEM	3106	POTENTIAL.
					FT	TRANSMEM	3144	POTENTIAL.
					FT	TRANSMEM	3182	POTENTIAL.
					FT	TRANSMEM	3220	POTENTIAL.
					FT	TRANSMEM	3258	POTENTIAL.
					FT	TRANSMEM	3296	POTENTIAL.
					FT	TRANSMEM	3334	POTENTIAL.
					FT	TRANSMEM	3372	POTENTIAL.
					FT	TRANSMEM	3410	POTENTIAL.
					FT	TRANSMEM	3448	POTENTIAL.
					FT	TRANSMEM	3486	POTENTIAL.
					FT	TRANSMEM	3524	POTENTIAL.
					FT	TRANSMEM	3562	POTENTIAL.
					FT	TRANSMEM	3600	POTENTIAL.
					FT	TRANSMEM	3638	POTENTIAL.
					FT	TRANSMEM	3676	POTENTIAL.
					FT	TRANSMEM	3714	POTENTIAL.
					FT	TRANSMEM	3752	POTENTIAL.
					FT	TRANSMEM	3790	POTENTIAL.
					FT	TRANSMEM	3828	POTENTIAL.
					FT	TRANSMEM	3866	POTENTIAL.
					FT	TRANSMEM	3904	POTENTIAL.
					FT	TRANSMEM	3942	POTENTIAL.
					FT	TRANSMEM	3980	POTENTIAL.
					FT	TRANSMEM	4018	POTENTIAL.
					FT	TRANSMEM	4056	POTENTIAL.
					FT	TRANSMEM	4094	POTENTIAL.
					FT	TRANSMEM	4132	POTENTIAL.
					FT	TRANSMEM	4170	POTENTIAL.
					FT	TRANSMEM	4208	POTENTIAL.
					FT	TRANSMEM	4246	POTENTIAL.
					FT	TRANSMEM	4284	POTENTIAL.
					FT	TRANSMEM	4322	POTENTIAL.
					FT	TRANSMEM	4360	POTENTIAL.
					FT	TRANSMEM	4398	POTENTIAL.
					FT	TRANSMEM	4436	POTENTIAL.
					FT	TRANSMEM	4474	POTENTIAL.
					FT	TRANSMEM	4512	POTENTIAL.
					FT	TRANSMEM	4550	POTENTIAL.
					FT	TRANSMEM	4588	POTENTIAL.
					FT	TRANSMEM	4626	POTENTIAL.
					FT	TRANSMEM	4664	POTENTIAL.
					FT	TRANSMEM	4702	POTENTIAL.
					FT	TRANSMEM	4740	POTENTIAL.
					FT	TRANSMEM	4778	POTENTIAL.
					FT	TRANSMEM	4816	POTENTIAL.
					FT	TRANSMEM	4854	POTENTIAL.
					FT	TRANSMEM	4892	POTENTIAL.
					FT	TRANSMEM	4930	POTENTIAL.
					FT	TRANSMEM	4968	POTENTIAL.
					FT	TRANSMEM	5006	POTENTIAL.
					FT	TRANSMEM	5044	POTENTIAL.
					FT	TRANSMEM	5082	POTENTIAL.
					FT	TRANSMEM	5120	POTENTIAL.
					FT	TRANSMEM	5158	POTENTIAL.
					FT	TRANSMEM	5196	POTENTIAL.
					FT	TRANSMEM	5234	POTENTIAL.
					FT	TRANSMEM	5272	POTENTIAL.
					FT	TRANSMEM	5310	POTENTIAL.
					FT	TRANSMEM	5348	POTENTIAL.
					FT	TRANSMEM	5386	POTENTIAL.
					FT	TRANSMEM	5424	POTENTIAL.
					FT	TRANSMEM	5462	POTENTIAL.
					FT	TRANSMEM	5500	POTENTIAL.
					FT	TRANSMEM	5538	POTENTIAL.
					FT	TRANSMEM	5576	POTENTIAL.
					FT	TRANSMEM	5614	POTENTIAL.
					FT	TRANSMEM	5652	POTENTIAL.
					FT	TRANSMEM	5690	POTENTIAL.
					FT	TRANSMEM	5728	POTENTIAL.
					FT	TRANSMEM	5766	POTENTIAL.
					FT	TRANSMEM	5804	POTENTIAL.
				</td				

DT 15-JUL-1998 (Rel. 36, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE chloride channel protein 4 (Clc-4).
 GN CLCN4 OR CLCN4-2 OR CLC4.
 OS MUS musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TAXID=10090;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C5BL/6J; TISSUE=Retina;
 RX MEDLINE-95400329; Published=7070496;
 RA Rigarli E.I., Adler D.A., Borsig G., Tsuchiya K., Franco B.,
 RA Hauge X., Disteche C., Chapman V., Bellabio A.;
 RT "Different chromosomal localization of the Clcn4 gene in *Mus spreitus*
 and C57BL/6J mice."
 RL Nat. Genet. 10:466-471(1995).
 CC -!- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
 SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
 TRANSEPITHELIAL TRANSPORT.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL: 249916; CA90150.1; -.
 DR MGI: 104571; Clcn4-2.
 DR InterPro: IPR00167; Cl-channel_volt.
 DR PFAM: PF00571; CBS; 2.
 DR SMART: S00016; CBS; 2.
 DR PRINTS: PRO00762; CLCHANNEL.
 DR KW IONIC CHANNEL; ION TRANSPORT; VOLTAGE-GATED CHANNEL; TRANSMEMBRAE;
 CBS domain; Repeat.
 FT TRANSMEM 55 75 POTENTIAL.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 189 209 POTENTIAL.
 FT TRANSMEM 246 265 POTENTIAL.
 FT TRANSMEM 317 337 POTENTIAL.
 FT TRANSMEM 352 372 POTENTIAL.
 FT TRANSMEM 429 449 POTENTIAL.
 FT TRANSMEM 454 474 POTENTIAL.
 FT TRANSMEM 495 515 POTENTIAL.
 FT DOMAIN 522 542 POTENTIAL.
 FT DOMAIN 586 646 POTENTIAL.
 FT DOMAIN 684 734 CBS 1.
 SQ SEQUENCE 747 AA; 83974 MW; B5486AA1B0721144 CRC64;

Query Match 77.0%; Score 3217; DB 1; Length 747;
 Best Local Similarity 77.6%; PScore. 1.5e-222; Matches 580; Conservative 83; Mismatches 84; Indels 0; Caps 0;

QY 45 LDDLDDEPIPGVGYDPTFHTDWKRKKDRERHRHRINSKKESAMENTKSLYDANSGWLW 104
 QY :|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 1 MDFFLEEPFPDVGYTEDFHTDWLRKEKSRTDHRKRITSKSRSIWEPIKSLIDAWNSGWVV 60
 Qy 105 VPLTGASLAGLGLIAADDMTDLKECIGCISALWNHEOCWGSMETTFERDKCPQWK 164
 Db 61 MLLGGLAGLTLAVDMDLKEGVCLSAFWYSHDOCWTTFEDRDKCPLWQ 120
 Qy 165 TWABLIGQAEGPSVIMNYIMWFLASFLAVLKVKVAPYAGCGSGIPEIKITLGF 224
 Db 121 KWSSELLLSQSISGASAYILNLYMLWALLFLAVSLVRLVRPAPYAGCGSGIPEIKITLGF 180 *

QY 225 IIRGYLGKWLTMKTTILVLAVASGLSIGREGPLVHVACCCGNIFSLFPKYSTNEAKR 284
 Db 181 IIIRGYLGKWLTMKTTILVLAVASGLSIGREGPLVHVACCCGNIFSLFPKYSTNEAKR 240
 QY 285 EVLSAASAGVSVAFGAPIGGLFSLEEVSYFPLKLWRSFAALVAFAVIRSINPFGN 344
 Db 241 EVLSAASAGVSVAFGAPIGGLFSLEEVSYFPLKLWRSFAALVAFAVIRSINPFGN 300
 QY 345 SRLVLVFVVEYHPTPWYLPELFPFLLGFGGGLGAFFRANTAWCRRKSTKGKPYLEV 404
 Db 301 SRLVLVFVVEYHPTPWYLPELFPFLLGFGGGLGAFFRANTAWCRRKSTKGKPYLEV 360
 QY 405 IIVAILTAIVAFPNPYTRNLNSLKEFTDCGPLESSICDYNMNAKLVDDIPDRP 464
 Db 361 IAVTAIVAVYAPNPYTRNSTSELISLENDGALESSOLODINDPNMTIPVDIDPDR 420
 QY 465 AGIGVVAISIWQGLALIFKRMIVFPTGIKRPSVGLFTPSMAIGAIGRIVGTAVEQLAY 524
 Db 421 ASGYVYTAIWQGLALIFKRMIVFPTGIKRPSVGLFTPSMAIGAIGRIVGTAVEQLAY 480
 CC 525 HRHDWFIFKEWCEVGACDCTPGLYAMVGAACLGCVTRMTVSLVTVFELTSLEYVPLM 584
 CC 361 AAATVSKWVAADAGKEGYIAHHLANGPFLDVKDEFTHRATLWDWRPREPPVSLT 600
 CC 481 HHDWI1FRNWRCRGADCVPLGIXAMVGAACLGCVTRMTVSLVTVFELTSLEYVPLM 540
 QY 585 AAVMTSKWVGAFREGCYEAHRLNGPFDAKEETHTLAADMVRPRNDPPLAVT 644
 Db 541 AAATVSKWVAADAGKEGYIAHHLANGPFLDVKDEFTHRATLWDWRPREPPVSLT 600
 QY 645 QDNMTVDIENNTNETSYNGFPVMSGESQRLYGFLARRDITAESARKOEGIVGSSR 704
 Db 601 QDSMTVEDVETUJKTEDYNGFVLUVDSERUJGFAQREL-LAIKNARQROEGIVNSI 660
 QY 705 VCFAQHAPSPLAESPRPLKLRSILDMSPPFTVDTHTPMETVUDIFRKLGRLRCVTHNGRL 764
 Db 661 MFTEEEPPLPANSPHPLKLRRIFNLSPPFTVDTHTPMETVUDIFRKLGRLRCVTHNGRL 720
 QY 765 LGITTKDIDLRIAMAQNQDASIMFN 791
 Db 721 LGITTKDIDLRIAMAQNQDASIMFN 747

RESULT 8

CIGS_HUMAN	ID	CIGS_HUMAN	STANDARD;	PRT;	746 AA.
AC PS1795;	AC				
DT 01-OCT-1996 (Rel. 34, Created)	DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)	DT				
DE Chloride channel protein 5 (Clc-5).	DE	CLCN5 OR CLK2.			
OS Homo sapiens (Human).	OS				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OC				
OX NCBI_TAXID=9606;	OX				
RN [1]	RN				
RP SEQUENCE FROM N.A.	RP				
RC TISSUE=Kidney;	RC				
RX MEDLINE-96121370; Published=8575751;	RX				
RA Fisher S.E., van Bakel T., Lloyd S.E., Pearce S.H.S.,	RA				
RA Thakker R.V., Craig I.W.;	RA	"Cloning and characterization of CLCN5, the human kidney chloride			
RT channel gene implicated in Dent disease (an X-linked hereditary	RT	nephrolithiasis);"			
RT Genomics 29:598-606(1995).	RT				
RN [2]	RN				
RP SEQUENCE OF 487-746 FROM N.A.	RP				
RC TISSUE=Kidney;	RC				
RX MEDLINE-95179126; PubMed=7874126;	RX				
RA Fisher S., Black G.C.M., Lloyd S.E., Hatchwell E., Wrong O.,	RA				
RA Thakker R.V., Craig I.W.;	RA	"Isolation and partial characterization of a chloride channel gene			
RT which is expressed in kidney and is a candidate for Dent's disease	RT	(an X-linked hereditary nephrolithiasis);"			

RL HUM. Mol. Genet. 3:2053-2059(1994).
 RN [3]
 TISSUE SPECIFICITY
 Tissue-vascular smooth muscle, and Aortic endothelium;
 MEDLINE:99222497; PubMed=10198195;
 RA Lamb F.S.; Clayton G.H.; Liu B.-X.; Smith R.L.; Barna T.J.;
 RA Schutte B.C.; Liu B.-X.; Smith R.L.; Barna T.J.;
 RT "Expression of CLCN voltage-gated chloride channel genes in human blood vessels";
 RL J. Mol. Cell. Cardiol. 31:657-666(1999).
 RN [4]
 RP VARIANTS NPHL ARG-200: LEU-244: GLU-506 AND PRO-520.
 RX MEDLINE:96158876; PubMed=8559248;
 RA Lloyd S.E.; Pearce S.H.S.; Fisher S.E.; Steinmeyer K.; Schwappach B.; Scheinman S.J.; Goodyer P.; Devoto M.; Ridgen S.P.A.; Wrong O.; Jentsch T.J.; Craig I.W.; Thakker R.V.;
 RA "A common molecular basis for three inherited kidney stone diseases";
 RT Nature 379:445-449(1996).
 RN [5]
 RP VARIANTS NPHL.
 RX MEDLINE:97402204; PubMed=9259268;
 RA Lloyd S.E.; Guenther W.; Pearce S.H.S.; Thomson A.; Bianchi M.L.; Bosio M.; Craig I.W.; Fisher S.E.; Scheinman S.J.; Wrong O.;
 RA Jentsch T.J.; Thakker R.V.;
 RT "Characterisation of renal chloride channel, CLCN5, mutations in hypercalcicuric nephrolithiasis (kidney stones) disorders";
 Hum. Mol. Genet. 6:1239-1239(1997).
 CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
 MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSEPITHELIAL TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN RENAL TUBULAR FUNCTION.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: KIDNEY. MODERATELY EXPRESSED IN AORTIC VASCULAR SMOOTH MUSCLE AND ENDOTHELIAL CELLS, AND AT A SLIGHTLY HIGHER LEVEL IN THE CORONARY VASCULAR SMOOTH MUSCLE.
 CC -!- DISEASE: DEFECTS IN CLCN5 ARE THE CAUSE OF FOUR DISORDERS OF HEREDITARY HYPERCALCIURIC NEPHROLITHIASIS (KIDNEY STONES), THAT HAVE BEEN REFERRED TO AS DENT'S DISEASE (DD), X-LINKED RECESSIVE NEPHROLITHIASIS (XRN), X-LINKED RECESSIVE HYPOPHOSPHATEMIC RICKETS (XLHR) AND IDIOPATHIC LOW MOLECULAR WEIGHT PROTEINURIA OF JAPANESE CHILDREN (JILP). ALL FOUR DISEASES REPRESENT RENAL TUBULAR DISORDERS. THEY ARE CHARACTERIZED BY LOW MOLECULAR WEIGHT PROTEINURO, HYPERCALCIURIA, NEPHROLITHIASIS (KIDNEY STONES) AND RENAL FAILURE. DD IS A FORM OF FANCONI SYNDROME (ALSO KNOWN AS X-LINKED RECESSIVE NEPHROLITHIASIS TYPE 2 (NPHL2)).
 CC -!- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
 CC -----
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 CC -----
 DR Genew; HGNC: 2023; CLCNS.
 DR Pfan: PR00571; CBS; 2.
 DR Pfan: PR00654; voltage; CLC; 1.
 DR PRINTS; PR00762; CLCHANNEL.
 DR SMART; SM00116; CBS; 2.
 DR InterPro; IPR000644; CBS_domain.
 DR InterPro; IPR001807; Cl-channel_volt.
 DR EMBL; X18361; CAA57430_1; .
 DR GeneID: 300008; .
 DR MIM: 310468; .
 DR InterPro; IPR000644; CBS_domain.
 DR InterPro; IPR001807; Cl-channel_volt.
 DR Pfan: PR00571; CBS; 2.
 DR Pfan: PR00654; voltage; CLC; 1.
 DR PRINTS; PR00762; CLCHANNEL.
 DR SMART; SM00116; CBS; 2.
 KW Ion channel; Ion transport; Voltage-gated channel; Transmembrane; CBS domain; Repeat; Disease mutation.
 FT TRANSMEM 133 153
 FT TRANSMEM 189 209
 FT TRANSMEM 246 266
 FT TRANSMEM 317 337
 FT TRANSMEM 352 372
 FT TRANSMEM 428 448
 FT TRANSMEM 453 473
 FT TRANSMEM 494 514
 FT TRANSMEM 521 541
 FT DOMAIN 585 645
 FT DOMAIN 682 733
 FT VARIANT 30 30
 FT VARIANT 30 30
 FT VARIANT 57 57
 FT VARIANT 200 200
 FT VARIANT 506 506
 FT VARIANT 244 244
 FT VARIANT 280 280
 FT VARIANT 520 520
 FT VARIANT 527 527
 FT SEQUENCE 746 AA: 83146 MW: EF913CSBAA40C85D8 CRC64:
 QY 45 LDLDDEPFPGVGYDDFHTIDWREKDRERRHRRINSKKKESAWEMTKSLIDAWSGHLV 104
 Db 1 MDFELEEPFPGVGTVDDEFNTDWREKSRDRHREITNKSKESTWALTHSVSDFASGWLL 60
 QY 105 VTLIGLGLASGALAGLIDIAADWMTDLKEGICLSSALWYNHEQCCMGSNETTEFEERDKCPWKL 164
 Db 61 MLLIGLSSLQSLAGLIDISAHWWMDLKEGICLGGFWPNIEHCWNSEHVTFEERDKCPWKL 120
 QY 165 TWABLITIGGAEGREGSYIMYIMTFWALSAFLAVSLVKVAFAYACGSSGPIEKTLISGF 224
 Db 121 SWSSQLISTSDDEGARAYINVFMLWALLFAFLAVSLVKVAFAYACGSSGPIEKTLISGF 180
 QY 225 IIRGYLGKWLTMKTTIUVLAVASGLSLGKGEGPLVHACCGNIFSYLEPKYSTNEAKKR 284
 Db 181 IIRGYLGKWLTMKTTIUVLAVASGLSLGKGEGPLVHACCGNITCHCFNKYRKNEAKRR 240
 QY 285 EVLSASAAGWSVAFAGPIGGVIFSVLSLEEVSYYYPLKTIWRSFFAALVAFAFVRSINPGN 344
 Db 241 EVLSASAAGWSVAFAGPIGGVIFSVLSLEEVSYYYPLKTIWRSFFAALVAFAFVRSINPGN 300
 QY 345 SRLVLFYVVEHTPWLFELPFITLGVLGVGLCAFFTRANTAMCRRKSTKGKPYVLE 404
 Db 301 SRLVLFYVVEHTPWLFELPFITLGVLGVGLCAFFTRANTAMCRRKSTKGKPYVLE 360
 QY 405 IIVAITAVTFNPYTRINTSELKELEPFTDCGPLESSICDVRNDMANKTVDDIPRP 464
 Db 361 LIVVTAITAILAFPMNEYTRMSTSSELSEFLNDCGLDSSKLCDOYENRENTSK-GGELPDPR 419
 QY 465 AGIGVYSATWQLCLALIKIIMVFTFGIKVFSGLFIPSMAIGAIAGRIVGAVEQIAY 524
 Db 420 AGIGVYSATWQLCLALIKIIMVFTFGIKVFSGLFIPSMAIGAIAGRIVGAVEQIAY 479
 QY 525 HDWDFIKREWCEVGADCTPGLYAMVGAACLGGVTRMTVSLSVWIVFELTGLEYVPLM 584
 Db 480 HQETVFNWSCSOGACTPGLYAMVGAACLGGVTRMTVSLSVWIVFELTGLEYVPLM 539

Db	540	AAAMTSKWWADALGREGIYIHLIRLNGYPFLEAKEFAHKTLAMDVMKPRRNDPLVLT	644
Db	540	AAAMTSKWWADALGREGIYIHLIRLNGYPFLEAKEFAHKTLAMDVMKPRRNDPLVLT	599
Qy	645	QDNMTVDIENMINETSYNQFPVMSKESQVLGEFLRLRDLTIESARKKQEGIVGSSR	704
Db	600	QDSMTVEDVETITSETTYSGFPVVVSRESQRLVGFLRDLTIESARKKQEGIVGSSR	659
Qy	705	VCAQHPTSLPAPESPPRPLRSILDMSPTVTDTMPEIVWDIFRKIGLROCLVTHNGRL	764
Db	660	LYFTERSPPMPYPTPTKLRLNLDSPFTVTDLTPMEIVWDIFRKIGLROCLVTHNGRL	719
Qy	765	LGIITKKDIRLIMAQTANQDPASIMFN	791
Db	720	LGIITKKDVKHLQAQNODPSILEN	746
RESULT	9		
CLC5_RAT			
ID			
CLC5_RAT	STANDARD;	PRT:	746 AA.
AC	P51796; P70642;		
DT	01-OCT-1995 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Chloride channel protein 5 (CLC-5).		
GN	CLCN5.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	[1]		
RN	J.Biol.Chem. 270:31172-31177(1995). [2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	Medline=9512510; PubMed=8537381;		
RA	Steinmeyer K., Schwappach B., Bens M., Vandewalle A., Jentsch T.J.;		
RT	"Cloning and functional expression of rat CLC-5, a chloride channel related to kidney disease";		
RT	R.L. J.Biol.Chem. 270:31172-31177(1995).		
RR	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RX	Medline=9621536; PubMed=8626585;		
RA	Sakamoto H., Kawasaki M., Uchida S., Sasaki S., Marumo F.;		
RT	"Identification of a new outwardly rectifying Cl- channel that belongs to a subfamily of the CLC Cl- channels. ";		
RL	J.Biol.Chem. 271:10210-10216(1996).		
CC	- - - FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME; MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSPORTER-TRANSPORT. MAY PLAY AN IMPORTANT ROLE IN RENAL TUBULAR FUNCTION.		
CC	- - - SUBCELLULAR LOCATION: Integral membrane protein.		
CC	- - - TISSUE SPECIFICITY: KIDNEY-SPECIFIC.		
CC	- - - SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.		
CC	- - - SIMILARITY: CONTAINS 2 CBS DOMAINS.		
CC	- - -		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).		
Db	405	IIVAAITAVIAFPNPYRLNTSLIKEFLDCGPLESSLCDYRNDMASKTVDDIPDRP	464
Db	361	IIVTAATIAFLARPNEYTRMSTSELISELFNDCGILDSKLCDVHENHTSK-GGELPDRP	419
Qy	425	AGIVVYAIWQCLALFKIIMTVFTGIVKVPSSGLFIPSMATGAIGRIVGIAVEQLAYY	524
Db	420	HIDWTFIKEWCIVGACDCITPGIVYAMGVAACIGGVTRMVSIVVFLTGLEYTPML	584
Db	480	HIDWTFIKEWCIVGACDCITPGIVYAMGVAACIGGVTRMVSIVVFLTGLEYTPML	539
Qy	585	AAVMTSKWWDAFGREGIEAHIRLNGYPFLEAKEFAHKTLAMDVMKPRRNDPLVLT	644
Db	540	AAAMTSKWWADALGREGIYIHLIRLNGYPFLEAKEFAHKTLAMDVMKPRRNDPLVLT	599
Qy	645	QDNMTVDIENMINETSYNQFPVMSKESQVLGEFLRLRDLTIESARKKQEGIVGSSR	704
Db	600	QDSMTVEDVETITSETTYSGFPVVVSRESQRLVGFLRDLTIESARKKQEGIVGSSR	659
Qy	705	VCAQHPTSLPAPESPPRPLRSILDMSPTVTDTMPEIVWDIFRKIGLROCLVTHNGRL	764
Db	765	LGIITKKDIRLIMAQTANQDPASIMFN	791
Db	720	LGIITKKDVKHLQAQNODPSILEN	746
KW	CBS domain; Repeat.	55	POTENTIAL.
FT	TRANSMEM	133	POTENTIAL.
FT	TRANSMEM	189	POTENTIAL.
FT	TRANSMEM	246	POTENTIAL.
FT	TRANSMEM	317	POTENTIAL.
FT	TRANSMEM	352	POTENTIAL.
FT	TRANSMEM	428	POTENTIAL.
FT	TRANSMEM	453	POTENTIAL.
FT	TRANSMEM	494	POTENTIAL.
FT	TRANSMEM	521	POTENTIAL.
FT	DOMAIN	614	CBS 1.
FT	CONFFLICT	315	H -> Y (IN REF. 2).
SO	SEQUENCE	746 AA;	83067 MW;
			5F17D45F397003CE CRC64;
Query Match		75.1%; Score 3138.5; DB 1; Length 746;	
Best Local Similarity		76.6%; Pre. No. 6.3e-217;	
Matches		572; Conservative 86; Mismatches 88; Indels 1; Gaps	
Qy	45	IDLDEDEPIPGVGVYDFHTIDAWREKKDRERHRINSKKKESAWEMTSKLYDAWSGMV	104
Db	1	MDFLEPEIPGVGVYDFHTIDAWREKSRRDRREITNSKESTWALHSVSDAFSGNL	60
Qy	105	VITLGAGLAGLIDITADWMMDLKEGICLSSLWYNHEQCCGSSNETTEFEERDKCPNK	164
Db	61	MULLIGLUSLAGLIDISAHWMPLDKEGICLCTGGFWNEHCWNSEHTEFDKCPNW	120
Qy	165	TWAELLIQOAEGPSYNNYIMVIFWALSFAFLAVSLVKFARYAACGSGIPEIKTLISGF	224
Db	121	SNSQLIISTDQGAFAYTINYFMVWLWALLFAFLAVSLVKFARYAACGSGIPEIKTLISGF	180
Qy	225	ITRGYIWKWLMIKTTILWLVASGLSLKGKEGLPVWVACCGNIFSVLPKYSTEAKKR	284
Db	181	ITRGYIWKWLVIKTITLWLVASSGLSLKGKEGLPVWVACCGNITCHCFNKYKRNEAKRR	240
Qy	285	EVLSASAKAGVSVAFGAPIGGIVLFSLEEVSYFPPLKTIWRSFFAALVAFVLESINPPGN	344
Db	241	EVLSAAGAGVSVAFGAPIGGIVLFSLEEVSYFPPLKTIWRSFFAALVAFVLESINPPGN	300
Qy	345	SRILVLFVYEHPTWYFLFELPFITLGVFGGLMAGFIRNTANCRRKSTKFGKPYVLE	404
Db	301	SRILVLFVYEHPTWYFLFELPFITLGVFGGLMAGFIRNTANCRRKSTKFGKPYVLE	360
Qy	405	IIVAAITAVIAFPNPYRLNTSLIKEFLDCGPLESSLCDYRNDMASKTVDDIPDRP	464
Db	361	IIVTAATIAFLARPNEYTRMSTSELISELFNDCGILDSKLCDVHENHTSK-GGELPDRP	419
Qy	465	AGIVVYAIWQCLALFKIIMTVFTGIVKVPSSGLFIPSMATGAIGRIVGIAVEQLAYY	524
Db	420	HIDWTFIKEWCIVGACDCITPGIVYAMGVAACIGGVTRMVSIVVFLTGLEYTPML	584
Db	480	HIDWTFIKEWCIVGACDCITPGIVYAMGVAACIGGVTRMVSIVVFLTGLEYTPML	539
Qy	585	AAVMTSKWWDAFGREGIEAHIRLNGYPFLEAKEFAHKTLAMDVMKPRRNDPLVLT	644
Db	540	AAAMTSKWWADALGREGIYIHLIRLNGYPFLEAKEFAHKTLAMDVMKPRRNDPLVLT	599
Qy	645	QDNMTVDIENMINETSYNQFPVMSKESQVLGEFLRLRDLTIESARKKQEGIVGSSR	704
Db	600	QDSMTVEDVETITSETTYSGFPVVVSRESQRLVGFLRDLTIESARKKQEGIVGSSR	659
Qy	705	VCAQHPTSLPAPESPPRPLRSILDMSPTVTDTMPEIVWDIFRKIGLROCLVTHNGRL	764
Db	765	LGIITKKDIRLIMAQTANQDPASIMFN	791
Db	720	LGIITKKDVKHLQAQNODPSILEN	746

```

Db 61 MLLIGLGSLAGLIDISAHWMTDLKEGIC
QY 165 TWAELITIQOREGGPSYIMMIVIFWALSF
: : : : : : : : : : : : : : : : : : : : :
Db 121 SWAQOLINTPDQAFAYIVNWMYUWALLE
QY 225 IIRGYLGKWMIMIKITLVAVASGLSGK
: : : : : : : : : : : : : : : : : : : : :
Db 181 ITRGYLGKWLVIKITYLVAVSSGLSLCK
QY 285 EVLSAASAAGSVSVAVGAPAGGIVFSLREVS
: : : : : : : : : : : : : : : : : : : : :
Db 241 EVLSAASAAGSVSVAVGAPAGGIVFSLREVS
QY 345 SRLVLFYVEHTPWYLFLFPFLGILGVGG
: : : : : : : : : : : : : : : : : : : : :
Db 301 SRLVLFYVEHTPWHLFELVPFLVIGIFG
QY 405 IIVAAITAVAFAPNYYTRANTSELKLFPT
: : : : : : : : : : : : : : : : : : : : :
Db 361 LIVTAATLAFFPNEYTRKTSSELSELFN
QY 465 AGIGYSAWMCOLCLALIFTIMVFTFCIK
: : : : : : : : : : : : : : : : : : : : :
Db 420 HHDWLFKWECEVGADCTPFLGLYAMVGAAGA
QY 525 HHDWLFKWECEVGADCTPFLGLYAMVGAAGA
: : : : : : : : : : : : : : : : : : : : :
Db 480 HHDWGLFNSNCSQGADCITPFLGLYAMVGAAGA
QY 585 AAUVTSKWQDAFREGIVEAHLRNGPPF
: : : : : : : : : : : : : : : : : : : : :
Db 540 AAUVTSKWQDAFREGIVEAHLRNGPPF
QY 645 QDNMVYDDEBNMHNITSYNGFPIVMSKSO
: : : : : : : : : : : : : : : : : : : : :
Db 600 QDSMTVEDVDMITTSBTYSGFPVVVSRSQ
QY 705 VCFQAQHTPS1PAESPRPLKLRSILDMSFPT
: : : : : : : : : : : : : : : : : : : : :
Db 660 IYFTBHSPHPYPPVAPTLKRNTLDLSP
QY 765 LGIITKKDRIRHMQATONODPASIMFN 79
: : : : : : : : : : : : : : : : : : : : :
Db 720 LGIITKKDRIRHMQATONODPASIMFN 79
QY 720 LGIITKKDRIRHMQATONODPDSILEN 74

```

RESULT 11

GEF1 YEAST	STANDARD;	PRT;
AC P37020;	DT 01-JUN-1994 (Rel. 29, created)	DT 15-JUN-2002 (Rel. 41, last annotation)
DE GEF1 protein (Voltage-gated chloride channel protein)	GN GEF1 OR CLCY1 OR YJR040W OR J1616	OS <i>Saccharomyces cerevisiae</i> (Baker's yeast)
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes	OC Saccharomycetes; Saccharomyces cerevisiae	OC Saccharomyces; <i>Saccharomyces cerevisiae</i>
OX NCBI_TAXID=4932;	RN [1]	RC SEQUENCE FROM N.A.
RC STRAIN=S288C;	RC MEDLINE=94088447; PubMed=7505388;	RA Greene J.R., Brown N.H., Didomenico R.J.
RT "The GEF1 gene of <i>Saccharomyces cerevisiae</i> encodes a membrane protein; mutations in which iron-limited growth.", Mol. Gen. Genet. 241:542-553(1993).	RT [2]	RN SEQUENCE FROM N.A.
RC STRAIN=S288C;		

CC -----

CC !-- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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CC -----

CC EMBL; AF063101; AACI8832.1; JOINED.

CC EMBL; AF063098; AACI8832.1; JOINED.

CC EMBL; AF063100; AACI8832.1; JOINED.

CC MGD; MGI:1347048; CLCN7.

DR InterPro; IPR00664; CBS_domain.

DR InterPro; IPR001807; Cl-channel_volt.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF0054; voltage_CLC; 1.

DR PRINTS; PRO0762; CLCHANNEL.

KW SMART; SM00116; CBS; 2.

KW Ion channel; Ion transport; Voltage-gated channel; Transmembrane;

KW CBS domain; Repeat.

FT TRANSMEM 175 195 POTENTIAL.

FT TRANSMEM 126 146 POTENTIAL.

FT TRANSMEM 222 242 POTENTIAL.

FT TRANSMEM 290 310 POTENTIAL.

FT TRANSMEM 373 393 POTENTIAL.

FT TRANSMEM 410 430 POTENTIAL.

FT TRANSMEM 493 513 POTENTIAL.

FT TRANSMEM 516 535 POTENTIAL.

FT TRANSMEM 579 599 POTENTIAL.

FT DOMAIN 627 674 CBS 1.

FT DOMAIN 737 781 CBS 2.

SQ SEQUENCE 803 AA; 88712 MW; A7D6DA5791DAA48C CRC64;

Query Match 18.0%; Score 751; DB 1; Length 803;

Best Local Similarity 29.1%; Pred. No. 4; 2e-46;

Matches 249; Conservative 139; Mismatches 270; Indels 198; Gaps 38;

QY 26 RGTHTYMTNGGSINSSTHLDLIDDEPIPGVGYTD-----DFHTIDWVR-EKCK 72

Db 45 ROSHALFERTGOMMNVNEDDELPBVDPHPITPKPEIPHNKLISLYESLDYDNSENQ 104

QY 73 DRERHRRINNSKKESAWEMTKSLYDAWSGLWVWTGLASAGLAGLIDIAADWMTDLKEG 132

Db 105 FLEERRIN---HTAFTPVEI----KRWVICALIGILTGLVACFDIVVENLAGLKYR 155

QY 133 ICLSAWLYNHQOCQCMWSNEITFEERIKCPQWKWTAELIIGQAEGPQSYIMYIMYFWA- 191

Db 156 VI-----KDNIDKPTEK-----GGLSFSL-----LLWAT 179

QY 192 LSFALFLAVS--LKVFAPYAGCGSGIPEIKTIISGFIRGYGKWTMIKITITLVLAWS 249

Db 180 LNSAFVLVGSIVTAFEPVAAQSGIQPKICLNGWVPHVRLKTLVIVSGVILSVWG 239

QY 250 LSLGKGQGPLVIVACCGNIES-----YLFPKYSTNEAKKREVLSAASAAGV 295

Db 240 LAVKGKEGPMIH---SGSVIAAGISQGRSTSLSKRDIFKIFKEYFRRDTETKRDFVSGAGAGV 295

QY 296 SVAFGAPIGGILFLSLEEVSYVFLPLKLIWRSFAALVAFAFLRSINPP-GN----SRL 347

Db 296 SAAFGAPVGVLFSLEEGASWNQFLTWRIFFASMISTFTNLVFLSYHGNMDLSSPGL 355

QY 348 VLF--VVEYHPTWYELFPRILLGVFGGMGAFFTRANTIAWCRRKSTKRG-KY---- 399

Db 356 INFGREDSEKMYTHIEPVFTAMGVGGTIGAVENALNYWL----TMFRIRYHRPC 409

QY 400 -PYLEVITVIAITAVTFAPPNTYTRLNTSELIKEFLFDGPLESSL-----C---D-YR 448

Db 410 LQVTEAMLVAATVAFVLISS-----RDCOPLOGSSMSYPLQLFCADGEY- 457

QY 449 NDMMAS-----KIVDDIPRPAGIGVYSAIWQCLGIALRIIMVTFTGKVPMSGFLI 501

Db 458 NSMAAFFNTPERSVSVLFHDPP--GSPNPMILGFLTVY-FFLACWVYGTIVSAGVFI 513

QY 502 PSMALGALAGRIVGIAVNEQOLAYVHHDWIFKBNCEVGACDCTPGLYMMGAAACLGVTR 561

Db 514 PSLLGAAWGRIGLFGISLISLYT-----GAIAWAD--PGKYLAMGAAQOLGSIYR 559

Db 562 MTSLVWVFLPTEGGLEITVPMAMVTSKWAQDAAFRGREGIEBAHIRNGYRPLDABEF 621

Db 560 MTLSLTVMMEATSNNVYGFPIMLVLMKAKIVQDF-TEGLYDMHIOLOQSVPFLHWBAPV 618

QY 619 TSLSLTAERVM---STPVTCILR-REKVGITDVLSLSDTASNHNHGPFVVEDGDTQPAR 672

Db 622 T-HTTLAADMVRPRRNDDPPLAVITQDNMTDIDENMINET-SYNGFPVIM--SKESOR 675

QY 676 LVGFLAFLRDLTIAESARKKQBGIVGSSRVCFQH-----ISLPA----- 716

Db 673 LGQLLRSOLIVILL---KHKVVERNSNMGVLYQRRLRKDFRDAYAPRPPQIOSINVSQD 727

QY 717 ESPRPLKRSILSMSPEFTVDTHPMEVTDVFRKLRGQCLVHN-CRLGJITKDKILR 775

Db 728 ERCTMDLSEFMNPSPVTPVQEAISLPRVFKLFRALGLURHLVVVDNHNQVVGIVLTKDLR 787

QY 776 H-----MAQT 780

Db 788 YRLGKGGLEELSLAQ 803

RESULT 13

CLC7_RAT ID CLC7_RAT STANDARD; PRT; 803 AA.

AC P51799; DT 01-OCT-1996 (Rel. 34, Created)

AC P51799; DT 01-OCT-1995 (Rel. 34, Last sequence update)

AC P51799; DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Chloride channel protein 7 (Clc-7).

GN Rattus norvegicus (Rat).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TAXID=10116;

RN {1}

RP SEQUENCE FROM N.A.

RC TISSUE:Brain;

RX MEDLINE=96120311; Pubmed=8543009;

RA Braadt S., Jentsch T.J..

RT "Clc-6 and Clc-7 are two novel broadly expressed members of the CLC chloride channel family.";

RT FEBS Lett. 377:15-20(1995).

CC -!- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE

CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;

CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND

CC TRANSEPITHELIAL TRANSPORT.

CC -!- TISSUE SPECIFICITY: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: BRAIN, TESTIS, MUSCLE AND KIDNEY.

CC -!- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.

CC -----

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CC -----

CC EMBL; 267744; CAAI9157.1; -.

DR InterPro; IPR00544; CBS_domain.

DR InterPro; IPR001807; Cl-channel_volt.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF0054; voltage_CLC; 1.

DR PRINTS; PR00762; CLCHANNEL.

DR SMART; SM00116; CBS; 2.

OY 698 ----- -GIVGSSR----- -VCFFAQHTPSLPAESP 719
Db 713 RYPPYPNLYPDQSPSEDTMEERFRPUTFHGLRSQVLTVRGCVYSESQSS--ASQP 770
OY 720 R----- PLKRSILDM----- SPETVTDHMPMETVVDIFRKL 751
Db 771 RLSYAEMADYPRYPDIDLDLTLLNPRMIVDVTYPMNPSPFTVSPNTHSVSOVNLFRTM 830
OY 752 GLIQC-LVTHNGRLLGITKKDILRHMAQ 779
Db 831 GLRHLPLVNVAVGSGIVGILTRHNITYEFLQ 859

Search completed: May 12, 2003, 15:03:19
Job time : 31 secs